

FIGURE 1

ATGGCGGGGCGGACACGGGCGCGGGCTCCTGGTGCTGACCTTCTGCCTGCTGTCCGCG 60
 CGCGGGGAGCTGCCATTGCCCCAGGAGACAACCTGTCAAGCTGAGCTGTGATGAGGGACCC 120
 CTGCAAGTGATCCTGGGCCCTGAGCAGGCTGTGGTGCTGGACTGCACTTTGGGGGCTACA 180
 GCTGCTGGGCCTCCGACCAGGGTGACATGGAGCAAGGATGGAGACACTGTACTAGAGCAT 240
 GAGAACCTGCACCTGCTACCCAATGGCTCCCTGTGGCTGTCTCACCCTTAGAGCAAGAA 300
 GACAGCGATGATGAGGAAGCTCTTAGGATCTGGAAGGTCACCTGAGGGCAGCTATTCTGT 360
 CTGGCCCAAGCCCGCTAGGAGTGGTGGCCAGCCAGGTTGCTGTGGTCAAGCTTGCCACA 420
 CTCGAAGACTTCTCTGACCCCCAGTCCAGATTGTGGAGGAGAACGGGACAGCACGC 480
 TTTGAATGCCACACCAAGGGCCTTCCAGCCCCATCATTACTTGGGAAAAGGACAGGTG 540
 ACCGTGCTGAGGAGCCCCGGCTCATCACTCTTCCCAAGTGGCTCCTCCAGATCTTAGAT 600
 GTCCAGGACAGTGATGACGGCTCTACCGCTGCGTGCCACCAATTACGCCCGCCACGA 660
 TTCAGCCAGGAGGCTCGCTCACTGTGGCCCTCAGAGGGTCTTTGGAGGCTACCAGGGG 720
 CAGGATGTGGTCATTGTGGCAGCCCCAGAGAACACACGGTAGTGTCTGGACAGAATGTA 780
 GTGATGGAGTGCGTGGCCTCTGCTGACCCACCCCTTTTGTGTCTGGGTCCGACAGGAT 840
 GGAAAGCCTATCTCCACGGATGTCTGTTCTGGGCCGGACCAATCTACTCATCGCCAGC 900
 GCGCAGCCTCGGCACCTCTGGAGTCTATGTCTGCCGAGCCAACAAGCCCTCACGCGTGAC 960
 TTCGCCACTGCGGCTGCTGAGCTCCGAGTGCTTGTCTGCCCCAGCCATCTCGCAGGCACCC 1020
 GAGGCGCTCTCGCGGACGCGGGCCAGCACCGCGCGCTTCTGTGTCCGGGCGTCCGGGGAG 1080
 CCACGGCCCGCGCTGCACTGGCTGCACGACGGGATCCCGTTGCGACCCAATGGGCGCGTC 1140
 AAGGTGACGGGCGGTGGCGGCAGCTTGGTCTCACTCAGATCGGCCTGCAGGACGCTGGC 1200
 TACTACAGTGCGTAGCAGAAAACAGCGCGGGAAGTGCCTGTGCCCTGCGCCCCCTGGCG 1260
 GTAGTGTGCGCGAGGGGCTGCCCAGCGCCCCGACTCGGGTCACAGCCACGCCCGCTGAGC 1320
 AGCTCCTCTGTGCTGGTGGCCTGGGAGCGGCCTGAGTTGCACAGCGAGCAAATCATTGGC 1380
 TTCTCTCTTCACTACCAAAGGCAAGGGGAGTGGACAATGTGGAGTACCAGTTTGCAGTA 1440
 AACAATGACACCACAGAGCTGCAGGTTCCGGGACCTGGAACCCAACACGGATTATGAGTTC 1500
 TACGTGGTGGCCTACTCCCAGCTGGGGGCCAGCCGAACCTCCAGCCCAGCCCTGGTGCAT 1560
 ACCTGGACGATGTCCCAGCGCAGCACCCAGCTTACCTTGTCCAGCCCCAACCCCTCG 1620
 GACATCAGGGTGGCATGGCTGCCCCCTGCCCTCCAGCCTGAGCAATGGACAGGTGCTGAAG 1680
 TACAAGATAGAGTACGGTTTGGGGAAGGAAGATCAGGTTTCTCCACCGAGGTCCCTGGA 1740
 AATGAGACACAACCTACGTTAAACTCACTTCAGCCAAACAAGTGTACCGAGTCCGGATT 1800
 TCAGCTGGCACTGGCGCTGGCTATGGAGTCCCTTCTCAGTGGATGCAGCACAGGACACCT 1860
 GGTGTGCAACAACAGAGCCATGTTCCCTTTGCCCTGCAGAATTGAAGGTGAGGGCAAAG 1920
 ATGGAGTCCCTGGTGGTGTCTATGGCAGCCGCCCTCACCCACCCAGATCTCTGGATAC 1980
 AAATCTACTGGGAGAGGTGGGAACAGAGGAGGAGGCAGATGGTGACCGCCCCCAGGG 2040
 GGTCTGGAGATCAAGCTTGGGACGTCGGGCCGTGCGGCTGAAGAAGAAAGTGAAGCAG 2100
 TATGAAGTGAACCAAGTATGCTCCCTGGCAGGCCGTACGAGGTGAAGCTCGTAGCTTTCAAC 2160
 AAACACGAGGACGGCTACGCTGCTGTGTGGAAGGGCAAGACGGAGAAGGCGCCACGCCA 2220
 GACCTGCCTATCCAGAGGGGGCCACCGCTGCCTCCTGCCCATGTCCACGCAGAGTCAAAC 2280
 AGCTCCACTTCCATTTGGCTTCGGTGGGAAGAAGCCAGACTTTACCAGTGTCAAGATTGTC 2340
 AACTACACTGTACGCTTCGGCCCCCTGGGGGCTCAGGAATGCTTCCCTGGTCACCTACTAT 2400
 ACCAGCTCTGGAGAAGACATTCTCATTGGCGGCCTGAAACCATTTACCAAGTACGAGTTT 2460
 GCGGTACAGTCCACAGGAGTGATATGGATGGGCCCTTTGGCTCCGTCGTAGAACGCTCC 2520
 ACCCTGCCTGACCGGCCTTCAACACCTCCTTCTGACCTGCGCCTGAGCCCCCTGACACCA 2580
 TCCACCGTTCCGTTACACTGGTGTCCCCCACGGAGCCCAATGGTGAGATTGTGGAGTAT 2640
 CTAATCTCTACAGCAACAACCACACCCAGCCGAACACCAAGTGGACACTGCTCACCACA 2700
 GAGGGAACATCTTCAGTGCAGAGGTCCATGGCCTAGAGAGTGACACTCGGTATTTCTTC 2760
 AAGATGGGAGCCCGACAGAGGTGGGCCCTGGGCCCTTTTCCCGCTTGCAAGATGTGATT 2820
 ACTCTGCAAGAGACATTCTCAGACTCCTTGGATGTGCACGCGTCACGGGCATCATCGTG 2880
 GGTGTCTGCTGGGCCTTCTCTGCCCTCCTGGCCTGCATGTGTGCTGGCCTACGACAAAGC 2940
 TCCACAGGGAAGCCCTTCCCGGATTGTCTCCTCCTCAGGCACCCACAGGAAACCCAGCGCTC 3000
 TACACAAGAGCTCGGCTTGGGCCTCCAGTGTCCCTGCTGCCCATGAGTTGGAGTCCCTC 3060
 GTGCATCCTCGTCCCAGGATTGGTCCCCACCACCTCAGATGTGGAAGACAAGGCTGAA 3120
 GTACACAGCCTTATGGGTGGCAGTGTTCAGATTGCCGGGGCCACTCCAAGAGAAAGATC 3180
 TCCTGGGCTCAGGCAGGGGACCAAACTGGGCAGGCTCCTGGGCAGGCTGTGAGCTGCCC 3240
 CAGGGTAGTGGTCCAAGGCCGGCTCTGACCCGTGCTCTGCTGCCTCCAGCGGGAACCGGG 3300
 CAGACACTGCTGCTGCAAGCCCTGGTGTATGACGGCATAAAGAGCAACGGGAGAAAGAAG 3360
 CCGTCCCCAGCCTGCAGGAATCAGGTGGAAGCTGAGGTCATTGTCCACTCCGACTTCGGT 3420
 GCATCCAAAGGATGTCTGACCTCCACCTCCAAGACCTGGAGCCAGAGGAACCACTGACT 3480

FIGURE 2A

GCAGAGACTCTGCCCTTCCACGTCTGGAGCTGTGGATCTGTCTCAAGGAGCAGACTGGCTG 3540
GGCAGGGAGCTGGGAGGGTGCCAACCAACAACCAAGTGGGCCAGAGAGGCTCACCTGCTTG 3600
CCAGAAGCAGCCAGTGCCTCCTGCTCCTGCTCAGACCTCCAGCCCAGCACTGCTATAGAG 3660
GAGGCCCCCTGGGAAAAGCTGCCAGCCCAAAGCCCTGTGTCTCTAACAGTCAGCCCAAGC 3720
CTTCCCAGGGCCCCCTGTCTCCTCTGCTCAGGTCCCCCTGAGCAGAAGGCAGATATGGCTCA 3780
GGAACATGCCATGCATGGCTACACATGTGTGTACTAGAGATATCCATAAGTCTTGGAGC 3840
CTCTTAGGGTCTTTTGGCTGGGGTTGGGGAGAACTTTACTCTCCCTCATATTCTGCATCA 3900
CATACAGGAGGGACTTGAGACACAGCTCTGTGTAATGGACACGTGTGAAGTCGTGTGTGT 3960
GT 4020
GCCTAGTTGACCCTCCGTGGCAGGATGGTGTAAACAGTGATCAGTGCCAGCTCTTTGAGCT 4080
TTTAGCCTTGTCACCTAGCCTTTTATTACACTCTGAGAGTGTCTCCAGTGCTGTGTCTAC 4140
AAAGACAGCGCCCAGCCCTCTTCTGTCTAGCTGTGCTGAGCAGAGTGCCAGTCAACTCCAC 4200
GGGCCTATGACACCGCAGCCTACCAAGCATGGCTGTCTATCCCCCTGGCCTCCTAAGGTC 4260
CAGATGTCTGGGTGAACCCAGCTCAGCTCCCCCTCCTTTGAGCATCTCTGTACCTAATT 4320
TTGTAATCTGGGAAGTGCCCTGGTTTGGGAAATCTTCTTTTCGCACCCCTGTCCCTCTCTGCC 4380
CCTTCCTTCATTTGTTCTGGTGATCTGTCTCATGTCTATCTGCTCGATTATCCTGGGGCC 4440
CTTCTCTTTCCCATGATGCCCCCTGATTTCCCTCACTGCTGTTTTTCATTTCTGTCTGCCATG 4500
CTTGTCTTTATGTCTGTGTGTCTCTCGTCCCTGAGTTCAACCTATGCACCCTTTCTTAACA 4560
ACATGACTACCTCATGTCTGCTTCAGACCATAGTGTGACCCCTGGGTCCCCACAGCTCCC 4620
CTGCCAACCCTTCTTGGGCAGATGAGCCCACTCCAAGTAGATCTGGAAGAGCCCTTG 4680
TGGCTTGCTGTGGCTGCCCTCCCCCTTGGTGTGAGATGAGAAGGTTTTCTATGGAAGAGAT 4740
GAGTCCAGGCTGCACAGGGGAACCCCAAGAAGGGGTAGGGAGTGAAACCAAGAGGCTGA 4800
AAAAAATGGCTGCCACCCATCTGCACAGAGAGATGGGTGTGTGCTTTTGACGTGCAGTC 4860
CTGGCTGAAACTGAAGGGGTGAGGAGAGGGGAGCTACTGGGGCTGCCATGGCTCAGTTCC 4920
CTGACCCTGGAGCCCTGAACCTGGCTTCAGAGTAGCAAAGAGTTTCTCCAAGATGCTGT 4980
AAGGGAAGTCTTTGCATAGGAAAAGGGCGGCTGGCTCATTTTATTTTATCTTTCTTTTACA 5040
CTGAATCCCAAATCATCTTACCACAAAGGGCCAAGCCTGACTGGTATTTCTGAGTCAC 5100
AAGAGCCATGCCATCTCTCTGGTTTCTCACCTCAGTCATGTCCAGAATTGTCTAGATCCA 5160
GTGGCATCTGTGCTCTTGTGTCACATCTTTCTATTTCAACTGGCTGGCAGATCAAGTGT 5220
AACTCTGGCTTCTGGGCCAAGTTAGAAATAACAGTCTATTTTCCCTTTATTTTATTTTA 5280
TTTTATTTTATTTTATGTCTTTTCTAGTGGAGTTGTAGCTTCTGAAAGCGTCTGTGTTTATT 5340
AGCCTTGCTGTGTCTACTCATGTTTGACCCCAACCATTTTCTCTCTCTCTCTCTCTCTCAGC 5400
CAGCCTATGATAACACTAAAGATTATTAATGCTGGCTTCGTATCTCATTAAGACAGGAT 5460
TGTCACTTGAACCTACTTCTATAGCATTCAAAGTGGCCACGGCCACACACACCGTATGTTT 5520
CTTCATGTCTCTGAAGGTCAAGAGCCTCATTTTGTTTTCTGGTTAGATTCTTTTCTCTCC 5580
TTGCCTTGAATGAAATAACCGTTTAAACAGTAGGCTCTTAGCATCACACCACATAGTCAT 5640
TCCTCATGTTCTTGTTTAACAAGCACTTGAGGTTCTGGGTTTAAATTAAATAGCTGCAAA 5700
TGAGACAATTTATAACCCATTAGGCTGGGTGGAAAATTGTTCTCAAAAGCAAATAAGTAA 5760
TAAATCTGGTATCTGCCTATAACTCACAGTTGATAAGAAAGTAGCCAGAAGTCACTAGCA 5820
TTATATATGATTGGGGTTCTGAGTAAGTGGGGAGTGTTAGCTTTGTGACTTTGTAGCACC 5880
AGGTCTTATTAGGAAAGTCTGTTGGCCTTTTACAGGGCATTAGTCCCTTTGTGCTTTGCC 5940
ATGGATGCCTTAAGTTCTTTGGAGTCTCATTTAAGAATTCTTTTCTCGAAGCATGACAA 6000
GTGTATCGCAATACTTACATGCTCACTCGTTTACCTGGCTTAGTTTGTGCTGGGTTATTT 6060
AATTGCACTTTCCAGCATCATGCTTCTCCTTACAAATATGATATCTTTATTGTTACAC 6120
TAAGGTGTTGATCATGTATCTGTCCCTGTAAAGAATTAATAAACTATTTTCCAGAC 6176

FIGURE 2A

10	20	30	40	50	60	70	80
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MARADTGRGLLVLTFCLLSARGELPLQETTVKLSCDEGPLQVILGPEQAVVLDCTLGATAAGPPTRVTWSKGDVLEH
ENLHLLPNGSLWLSPPLEQEDSDDEEALRIWKVTEGSYCLAHSPLGVVASQVAVVKLATLEDFSLHPESQIVEENG TAR
FECHTKGLPAPIITWEKDQVTVP EEPRLITLPKWLQILDVQSDAGSYRCVATNSARQFSQEASLTVALRGSLEATRG
QDVVIVAAPENTTVVSGQNVVMECVASADPTPFVSWVRQDGKPISTDVIVLGRTNLLIASAQPRHSGVYVCRANKPLTRD
FATAAAELRVLAAPASQAPEALSRTASTARFVCRASGEPRPALHWLHDGIPLRPNGRVKVQGGGSLVITQIGLQDAG
YYQCV AENSAGTACAAAPLAVVREGLPSAPTRVTATPLSSSSVLVAWERPELHSEQIIGFSLHYQKARGVDNVEYQFAV
NNDTTELQVRDLEPNTDYEFYVAYSQLGASRTSSPALVHTLDDVPSAAPQLTLSSPNPSDIRVAWLPLPSSLNQGVLK
YKIEYGLGKEDQVFSTEVPNETQLTLNSLQPNKVYRVRI SAGTGAGYGVPSQWMQHRTPGVHNQSHVPFAPAE LKVRAG
MESLVVSWQPPPHPTQISGYKLYWGEVGTEEEADGDRPPGGRGDQAWDVGPVRLKKVKQYELTQLVPGRPYEVKLVAFN
KHEDGYAAVWKGKTEKAPTDLPIQRGPPLPPAHVHAESNSSTSIWLRWKKPDFTTVKIVNYTVRFGPWGLRNASLV TYY
TSSGEDILIGGLKPFTKYEFVQSHGVMDGPF GSVVERSTLPDRPSTPPSDLRLSPLTPSTVRLHWCPTPEPNGEIVEY
LILYSNNHTQPEHQWTLTTTEGNIFSAEVHGLESDTRYFFKMGARTEVGPGPFSRLQDVITLQETFSDSLDVH
AVIGGV
GYGHELEEFACVAGLRQSSHREALPGLSSSGTPGNPALYTRARLGPPSVPAHELESLVHPRPDWSPPPSDVEDKAE
VHSLMGGSVSDCRGHSKRKISWAQAGGNWAGSWAGCELPQGSGRPALTRALLPPAGTGQTL LLQALVYDGIKSNRKK
PSPACRNQVEAEVIVHSDFGASKGCPDLHLQDLEPEEPLTAETLPSTSGAVDL SQGADWLGRELGGCQPTTSGPERLTCL
PEAASASCSCSDLQPSTAIIEAPGKSCQPKALCPLTVSPSLPRAPVSSAQVP

FIGURE 2B

10 20 30 40 50 60
 1 AGGCTGGTGGCGCGCGGGCGCGTGTCCCCTGTGGTGCAGGGTGGCCACACTGGCGGGGCG
 61 CCCCCGCGTGGGCGCTAGCCCAAGATGGCGATGGAGGGGCGGGCGAGCTGGCCGCGGCC
 121 CCGGCCCCCGCGCCGGCCCCCGCTCGGCCCCGGCCCCGGAGGCCCGCGCCCCGCGCGG
 181 CGCCGCGCCTCCCGAGCCACTGACGCCCGCGCGCCCTCCCCCGGCGGCGGCCAGGCG
 MetAlaArgAlaAspThrGlyArgG
 241 CCCGGACGCGGCGGCAGCGCCCCGAGCCCGGCCCTATGGCGCGGGCGGACACGGGCCGCG
 splice
 site
 | intron 1 >>
 lyLeuLeuValLeuThrPheCysLeuLeuSerAlaArg |
 301 GGCTCCTGGTGTGCTGACCTTCTGCCTGCTGTCCGCGCGCGGTAAGGGCCCGGGTGGCCGCA
 361 GTCGCGAGTGGGCGTCCCCGGCGCCCGCATGCTTGCGCGCCGGGGGCTGTGGGGACTTG
 421 CCCCCAGGGGGTGTGTGTCCTTGCTGTGCACAGCCTGGCACCGTGCGTGTCCCCCTGCGC
 481 GTGGCCCTTGTGCATGTGAG

FIGURE 2C

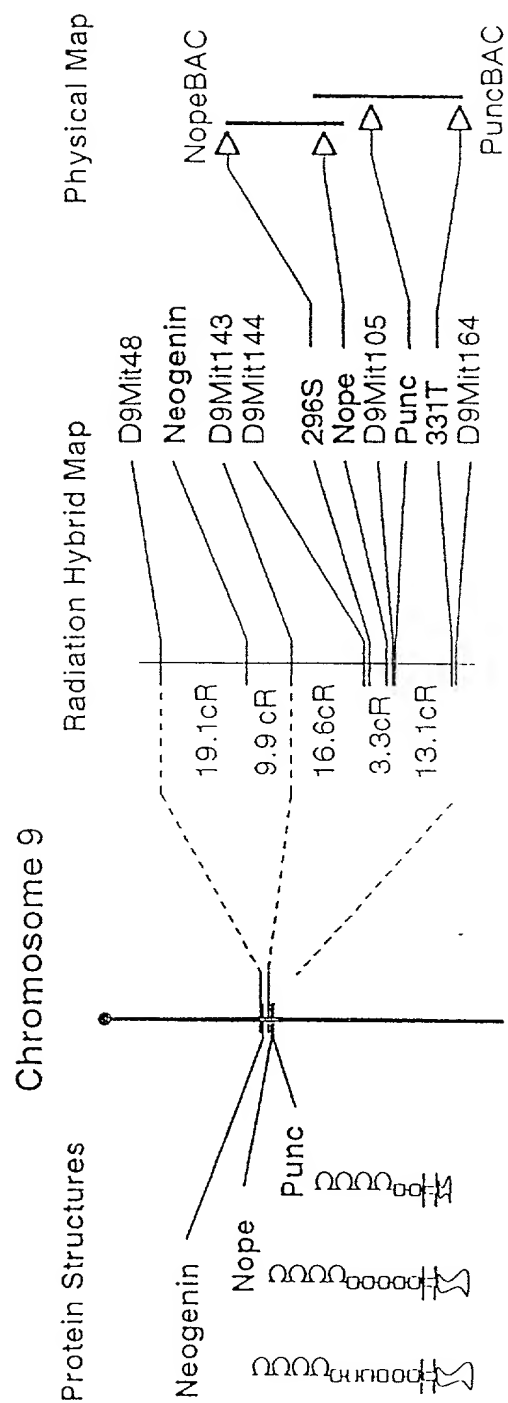


FIGURE 4